

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/578,840
Source: PG
Date Processed by STIC: 5/22/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/578,840

DATE: 05/22/2006

TIME: 14:19:19

Input Set : A:\060641-0113sequencetext.txt

Output Set: N:\CRF4\05222006\J578840.raw

2 <110> APPLICANT: Chugai Seiyaku Kabushiki Kaisha
W--> 3 <120> TITLE OF INVENTION: Humanized anti-CD47 antibody
W--> 4 <130> FILE REFERENCE: YCT-971
C--> 5 <140> CURRENT APPLICATION NUMBER: US/10/578,840
C--> 5 <141> CURRENT FILING DATE: 2006-05-10
W--> 5 <160> NUMBER OF SEQ ID: 92

ERRORED SEQUENCES

441 <210> SEQ ID NO: 32
442 <211> LENGTH: 130
443 <212> TYPE: DNA
444 <213> ORGANISM: Artificial Sequence
W--> 445 <220> FEATURE:
W--> 446 <223> OTHER INFORMATION:
E--> 446 <400> SEQUENCE: (130) 32 (change to)
447 cagcagagggc caggccaatc tccaaggcgc ctaatttata aagtttccaa ccgattttct 60
448 ggtgtcccag acagattcag cggcagtggg tcaggcactg atttcacact gaaaatcagc 120
449 aggggtggagg 130
471 <210> SEQ ID NO: 35
472 <211> LENGTH: (23) 22 ← shown below
473 <212> TYPE: DNA
474 <213> ORGANISM: Artificial Sequence
W--> 475 <220> FEATURE:
W--> 476 <223> OTHER INFORMATION: → same error as above
E--> 476 <400> SEQUENCE: (23) 35 ←
E--> 477 ccaagcttc caccatgagg ctc (23) 22
479 <210> SEQ ID NO: 36
480 <211> LENGTH: 23
481 <212> TYPE: DNA
482 <213> ORGANISM: Artificial Sequence
W--> 483 <220> FEATURE:
W--> 484 <223> OTHER INFORMATION:
E--> 484 <400> SEQUENCE: (23) 36 ←
485 cgcggatcca ctcacgtttg atc 23
487 <210> SEQ ID NO: 37
488 <211> LENGTH: 412
E--> 489 (212) ← insert these mandatory numeric identifiers and
E--> 490 (213) responder
W--> 491 <400> SEQUENCE: 37
492 atg agg ctc cct gct cag ctc ctg ggg ctg cta atg ctc tgg gtc cca 48
493 Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro

-20

-15

-10

-5

insert these amino acid number

see pp 1-8
Suggestion: Consult
Sequence Rules
for valid format

Does Not Comply
Corrected Diskette Needed

(global error)

see p. 7 for error

exploration

↓
This error appears in many sequences

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Input Set : A:\060641-0113sequencetext.txt

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```

495 ggc tcc agt ggg gat gtt gtg atg act cag tct cca ctc tcc ctg ccc 96
496 Gly Ser Ser Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
497      -1 1      5      10
498 gtc acc ctt gga cag ccg gcc tcc atc tcc tgc aga tca agt cag agc 144
499 Val Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
500      15      20      25
501 ctt gtg cac agt aat gga aag acc tat tta cat tgg ttt cag cag agg 192
502 Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Phe Gln Gln Arg
503      30      35      40
504 cca ggc caa tct cca agg cgc cta att tat aaa gtt tcc aac cga ttt 240
505 Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Phe
506      45      50      55      60
507 tct ggt gtc cca gac aga ttc agc ggc agt ggg tca ggc act gat ttc 288
508 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
509      65      70      75
510 aca ctg aaa atc agc agg gtg gag gct gag gat gtt gga gtt tat tac 336
511 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
512      80      85      90
513 tgc tct caa agt aca cat gtt ccg tac acg ttt ggc cag ggg acc aag 384
514 Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys
515      95      100      105
516 ctg gag atc aaa cgt gag tgg atc cgc g 412
517 Leu Glu Ile Lys
518      110

```

773 <210> SEQ ID NO: 54

774 <211> LENGTH: 39

775 <212> TYPE: DNA

776 <213> ORGANISM: Artificial Sequence

W--> 777 <220> FEATURE:

W--> 778 <223> OTHER INFORMATION:

E--> 778 <400> SEQUENCE: ⑤ 54 ←

779 ggggtggaggc tgatgatgtt ggaatttatt actgctctc 39

960 <210> SEQ ID NO: 68

961 <211> LENGTH: ②④ 25 shown

962 <212> TYPE: DNA

963 <213> ORGANISM: Artificial Sequence

W--> 964 <220> FEATURE:

W--> 965 <223> OTHER INFORMATION:

W--> 965 <400> SEQUENCE: 68

E--> 966 aggtgtcgac tcccaggtgc agctg ②④ 25

984 <210> SEQ ID NO: 71

985 <211> LENGTH: ④⑤ 46

986 <212> TYPE: DNA

987 <213> ORGANISM: Artificial Sequence

W--> 988 <220> FEATURE:

W--> 989 <223> OTHER INFORMATION:

W--> 989 <400> SEQUENCE: 71

E--> 990 aaaaggaaaa gggccgctc attatttgat ctccagcttg gtcccc ④⑤ 46

992 <210> SEQ ID NO: 72

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/578,840

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Input Set : A:\060641-0113sequencetext.txt

Output Set: N:\CRF4\05222006\J578840.raw

```

993 <211> LENGTH: 15
994 <212> TYPE: DNA
E--> 995 <213> ← insert mandatory response
W--> 996 <400> SEQUENCE: 72
997 ggt ggc gga ggt tcc 15
998 Gly Gly Gly Gly Ser
999 1 5
1125 <210> SEQ ID NO: 77
1126 <211> LENGTH: 45
1127 <212> TYPE: DNA
E--> 1128 <213> ← insert mandatory response
W--> 1129 <400> SEQUENCE: 77
1130 ggt ggt ggt ggt tcc ggt ggt ggt gga tcc ggt ggt ggc gga tcc 45
1131 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1132 1 5 10 15
1395 <210> SEQ ID NO: 87
1396 <211> LENGTH: 36
1397 <212> TYPE: DNA
1398 <213> ORGANISM: Artificial Sequence
W--> 1399 <220> FEATURE:
W--> 1400 <223> OTHER INFORMATION:
W--> 1400 <400> SEQUENCE: 87
E--> 1401 gggcagtgcc caagactcct gatctacaaa gtttcc 36 ← insert
1403 <210> SEQ ID NO: 88
1404 <211> LENGTH: 37
1405 <212> TYPE: DNA
1406 <213> ORGANISM: Artificial Sequence
W--> 1407 <220> FEATURE:
W--> 1408 <223> OTHER INFORMATION:
W--> 1408 <400> SEQUENCE: 88
E--> 1409 tcattatttg atctcaagct tgggtcccctg gccaaac 37 ←
1412 <210> SEQ ID NO: 89
1413 <211> LENGTH: 708
1414 <212> TYPE: DNA
E--> 1415 <213> ← insert mandatory response
W--> 1416 <400> SEQUENCE: 89
1417 caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgcaggtt 60
1418 tcctgtaagg catctggata caccttcacc aaccatgtta ttcactggct ggcacaggcc 120
1419 cccgggcaat gccttgagtg gatgggatat atttatcctt acaatgatgg tactaagtat 180
1420 aatgagaagt tcaaggacag agtcacgatg acctcagaca cgtccatcag cacagcctac 240
1421 atggagttga gcagtctcag atctgacgac acggccgtct attattgtgc tagagggggt 300
1422 tactatactt acgacgactg gggccaagca accctggcca cagtctcgag tgggtggcgga 360
1423 ggttccgata ttgtgatgac tcagtctcca ctctccctgc ccgtcacccc tggagagccg 420
1424 gcctccatct cctgcagatc aagtcagagc cttgtgcaca gtaatggaaa gacctattta 480
1425 cattgggtatc tgcagaagcc aggccagtct ccaagactcc tgatctacaa agtttccaac 540
1426 cgattttctg gtgtcccaga cagattcagc ggcagtggtt caggcactga tttcacactg 600
1427 aaaatcagca ggggtggaggc tgatgatgtt ggaatttatt actgctctca aagtacacat 660
E--> 1428 gttccgtaca cgtttggtcg cgggaccaag cttgagatca aataatga 708 ←
1430 <210> SEQ ID NO: 90

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/578,840

DATE: 05/22/2006

TIME: 14:19:20

Input Set : A:\060641-0113sequencetext.txt

Output Set: N:\CRF4\05222006\J578840.raw

1431 <211> LENGTH: 234
 1432 <212> TYPE: PRT
 E--> 1433 <213> *← insert mandatory response*
 W--> 1434 <400> SEQUENCE: 90

1435	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1436	1				5					10					15	
1437	Ser	Val	Gln	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	His
1438				20					25					30		
1439	Val	Ile	His	Trp	Leu	Arg	Gln	Ala	Pro	Gly	Gln	Cys	Leu	Glu	Trp	Met
1440			35					40					45			
1441	Gly	Tyr	Ile	Tyr	Pro	Tyr	Asn	Asp	Gly	Thr	Lys	Tyr	Asn	Glu	Lys	Phe
1442		50				55					60					
1443	Lys	Asp	Arg	Val	Thr	Met	Thr	Ser	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
1444	65					70					75				80	
1445	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
1446				85					90					95		
1447	Ala	Arg	Gly	Gly	Tyr	Tyr	Thr	Tyr	Asp	Asp	Trp	Gly	Gln	Ala	Thr	Leu
1448			100					105					110			
1449	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val	Met	Thr	Gln
1450			115					120					125			
1451	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Pro	Gly	Glu	Pro	Ala	Ser	Ile	Ser
1452		130				135					140					
1453	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Lys	Thr	Tyr	Leu
1454	145				150						155				160	
1455	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Arg	Leu	Leu	Ile	Tyr
1456				165					170					175		
1457	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser
1458			180					185					190			
1459	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Asp
1460		195						200					205			
1461	Asp	Val	Gly	Ile	Tyr	Tyr	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr
1462		210				215						220				
1463	Phe	Gly	Cys	Gly	Thr	Lys	Leu	Glu	Ile	Lys						
1464	225					230										

1466 <210> SEQ ID NO: 91
 1467 <211> LENGTH: 708
 1468 <212> TYPE: DNA
 E--> 1469 <213> *← insert mandatory response* *see p. 5*
 W--> 1470 <400> SEQUENCE: 91

1471	caggtgcagc	tggtgcagtc	tggggctgag	gtgaagaagc	ctggggcctc	agtgcaggtt	60
1472	tcctgtaagg	catctggata	caccttcacc	aaccatgtta	ttcactggct	gcgacaggcc	120
1473	cctgggcaag	ggcttgagtg	gatgggatat	atcttcctt	acaatgatgg	tactaagtat	180
1474	aatgagaagt	tcaaggacag	agtcacgatg	acctcagaca	cgtccatcag	cacagcctac	240
1475	atggagttga	gcagtctcag	atctgacgac	acggccgtat	actattgtgc	tagagggggt	300
1476	tactatactt	acgacgactg	gggctgcgca	accctgggtca	cagtctcgag	tggtggcgga	360
1477	ggttccgata	ttgtgatgac	tcagtctcca	ctctccctgc	ccgtcaccct	tggagagccg	420
1478	gcctccatct	cctgcagatc	aagtcagagc	cttgtgcaca	gtaatggaaa	gacctattta	480
1479	cattggtatc	tgcagaagcc	cgggcagtcg	ccaagactcc	tgatctacaa	agtttccaac	540
1480	cgattttctg	gtgtcccaga	cagattcagc	ggcagtgggg	caggcactga	tttcacactg	600

RAW SEQUENCE LISTING

DATE: 05/22/2006

PATENT APPLICATION: US/10/578,840

TIME: 14:19:20

Input Set : A:\060641-0113sequencetext.txt

Output Set: N:\CRF4\05222006\J578840.raw

1481 aaaatcagca ggggtggaggc tgatgatgtt ggaatttatt actgctctca aagtacacat 660
 E--> 1482 gttccgtaca cgtttggcca ggggaccaag cttgagatca aataatga 708 ← insert
 1484 <210> SEQ ID NO: 92
 1485 <211> LENGTH: 234
 1486 <212> TYPE: PRT
 E--> 1487 <213> *insert mandatory response*
 W--> 1488 <400> SEQUENCE: 92
 1489 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1490 5 10 15
 1491 Ser Val Gln Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn His
 1492 20 25 30
 1493 Val Ile His Trp Leu Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 1494 35 40 45
 1495 Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe
 1496 50 55 60
 1497 Lys Asp Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
 1498 65 70 75 80
 1499 Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 1500 85 90 95
 1501 Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Cys Ala Thr Leu
 1502 100 105 110
 1503 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln
 1504 115 120 125
 1505 Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser
 1506 130 135 140
 1507 Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu
 1508 145 150 155 160
 1509 His Trp Tyr Leu Gln Lys Pro Gly Gln Cys Pro Arg Leu Leu Ile Tyr
 1510 165 170 175
 1511 Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 1512 180 185 190
 1513 Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Asp
 1514 195 200 205
 1515 Asp Val Gly Ile Tyr Tyr Cys Ser Gln Ser Thr His Val Pro Tyr Thr
 1516 210 215 220
 1517 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 1518 225 230
 E--> 1523 ① *delete*

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<210> 7

<211> 424

<212> DNA

<213> Mouse, Human

<400> 7

atg gaa tgg agc tgg ata ttt ctc ttc ctc ctg tca gga act gca ggt 48

Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 96

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

-1 1

5

10

← insert
these
numbers

same error in sequence 10, seq. 13, 16, 19,
22, 30, 40, 43, 46,
49, 52, 57, 64, 67, 73,
74, 78, 79,

7

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/578,840

DATE: 05/22/2006
TIME: 14:19:21

error explanation Input Set : A:\060641-0113sequencetext.txt
Output Set: N:\CRF4\05222006\J578840.raw

Use of <220> Feature (NEW RULES):

Sequence(s) __ are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223>

section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)

(Sec.1.823 of new Rules)

Seq#:1,2,3,4,5,6,8,9,11,12,14,15,17,18,20,21,23,24,25,26,27,28,29,31,32,33,34

Seq#:35,36,38,39,41,42,44,45,47,48,50,51,53,54,55,56,58,59,60,61,62,63,65,66

Seq#:68,69,70,71,75,76,80,81,82,83,84,85,86,87,88

delete brackets

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8

(Sequence Listing)

<110> Chugai Seiyaku Kabushiki Kaisha

VERIFICATION SUMMARY

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TIME: 14:19:21

Input Set : A:\060641-0113sequencetext.txt

Output Set: N:\CRF4\05222006\J578840.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:4 M:283 W: Missing Blank Line separator, <130> field identifier
L:5 M:270 C: Current Application Number differs, Replaced Current Application No
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:5 M:283 W: Missing Blank Line separator, <160> field identifier
L:11 M:283 W: Missing Blank Line separator, <220> field identifier
L:12 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:12 M:283 W: Missing Blank Line separator, <400> field identifier
L:12 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:12
L:21 M:283 W: Missing Blank Line separator, <220> field identifier
L:22 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:22 M:283 W: Missing Blank Line separator, <400> field identifier
L:22 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:22
L:31 M:283 W: Missing Blank Line separator, <220> field identifier
L:32 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial Sequence
L:32 M:283 W: Missing Blank Line separator, <400> field identifier
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:32
L:41 M:283 W: Missing Blank Line separator, <220> field identifier
L:42 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:42 M:283 W: Missing Blank Line separator, <400> field identifier
L:42 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:42
L:51 M:283 W: Missing Blank Line separator, <220> field identifier
L:52 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:52 M:283 W: Missing Blank Line separator, <400> field identifier
L:52 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:52
L:59 M:283 W: Missing Blank Line separator, <220> field identifier
L:60 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:60 M:283 W: Missing Blank Line separator, <400> field identifier
L:60 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:60
L:67 M:283 W: Missing Blank Line separator, <400> field identifier
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:73 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:100 M:283 W: Missing Blank Line separator, <220> field identifier
L:101 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:101 M:283 W: Missing Blank Line separator, <400> field identifier
L:101 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:101
L:108 M:283 W: Missing Blank Line separator, <220> field identifier
L:109 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial Sequence
L:109 M:283 W: Missing Blank Line separator, <400> field identifier
L:109 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:109
L:116 M:283 W: Missing Blank Line separator, <400> field identifier
L:120 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:122 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:149 M:283 W: Missing Blank Line separator, <220> field identifier
L:150 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>

ORGANISM:Artificial Sequence

L:150 M:283 W: Missing Blank Line separator, <400> field identifier

L:150 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:150

L:157 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY

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Input Set : A:\060641-0113sequencetext.txt

Output Set: N:\CRF4\05222006\J578840.raw

L:158 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
ORGANISM:Artificial Sequence
L:158 M:283 W: Missing Blank Line separator, <400> field identifier
L:158 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:158
L:165 M:283 W: Missing Blank Line separator, <400> field identifier
L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:198 M:283 W: Missing Blank Line separator, <220> field identifier
L:199 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial Sequence
L:199 M:283 W: Missing Blank Line separator, <400> field identifier
L:199 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:199
L:206 M:283 W: Missing Blank Line separator, <220> field identifier
L:207 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>
ORGANISM:Artificial Sequence
L:207 M:283 W: Missing Blank Line separator, <400> field identifier
L:207 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:207
L:214 M:283 W: Missing Blank Line separator, <400> field identifier
L:218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:220 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:247 M:283 W: Missing Blank Line separator, <220> field identifier
L:248 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence
L:248 M:283 W: Missing Blank Line separator, <400> field identifier
L:248 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:248
L:255 M:283 W: Missing Blank Line separator, <220> field identifier
L:256 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:18, <213>
ORGANISM:Artificial Sequence
L:256 M:283 W: Missing Blank Line separator, <400> field identifier
L:256 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:256
L:263 M:283 W: Missing Blank Line separator, <400> field identifier
L:267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:269 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:296 M:283 W: Missing Blank Line separator, <220> field identifier
L:297 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>
ORGANISM:Artificial Sequence
L:297 M:283 W: Missing Blank Line separator, <400> field identifier
L:297 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:297
L:304 M:283 W: Missing Blank Line separator, <220> field identifier
L:305 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
L:305 M:283 W: Missing Blank Line separator, <400> field identifier
L:305 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:305
L:312 M:283 W: Missing Blank Line separator, <400> field identifier
L:316 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:318 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:346 M:283 W: Missing Blank Line separator, <220> field identifier
L:347 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence
L:347 M:283 W: Missing Blank Line separator, <400> field identifier
L:347 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:347
L:354 M:283 W: Missing Blank Line separator, <220> field identifier
L:355 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:24, <213>

ORGANISM:Artificial Sequence

L:355 M:283 W: Missing Blank Line separator, <400> field identifier

L:355 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24,Line#:355

L:362 M:283 W: Missing Blank Line separator, <220> field identifier

L:363 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:25, <213>

ORGANISM:Artificial Sequence

VERIFICATION SUMMARY

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TIME: 14:19:21

Input Set : A:\060641-0113sequencetext.txt

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L:363 M:283 W: Missing Blank Line separator, <400> field identifier
L:363 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:363
L:370 M:283 W: Missing Blank Line separator, <220> field identifier
L:371 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:26, <213>
ORGANISM:Artificial Sequence
L:371 M:283 W: Missing Blank Line separator, <400> field identifier
L:371 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:371
L:378 M:283 W: Missing Blank Line separator, <220> field identifier
L:379 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
ORGANISM:Artificial Sequence
L:379 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:379
L:387 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:28, <213>
ORGANISM:Artificial Sequence
L:387 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:28,Line#:387
L:395 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>
ORGANISM:Artificial Sequence
L:395 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:395
L:406 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:30
L:408 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:30
L:436 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:31, <213>
ORGANISM:Artificial Sequence
L:436 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:436
L:446 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:130, <213>
ORGANISM:Artificial Sequence
L:446 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32
differs:130
L:446 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:446
L:476 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:35
differs:23
L:477 M:254 E: No. of Bases conflict, LENGTH:Input:23 Counted:22 SEQ:35
L:477 M:252 E: No. of Seq. differs, <211> LENGTH:Input:23 Found:22 SEQ:35
L:484 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:36
differs:23
L:489 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for
SEQ ID#:37
L:490 M:206 E: Mandatory field data missing, <213> ORGANISM
L:544 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:40
L:546 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:40
L:593 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:43
L:595 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:43
L:642 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46
L:644 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46
L:691 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:693 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:740 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52
L:742 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52
L:778 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:54
differs:5
L:805 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:57
L:807 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:57
L:886 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:64
L:888 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:64
L:935 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:67

L:937 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:67
L:966 M:254 E: No. of Bases conflict, LENGTH:Input:24 Counted:25 SEQ:68
L:966 M:252 E: No. of Seq. differs, <211> LENGTH:Input:24 Found:25 SEQ:68
L:990 M:254 E: No. of Bases conflict, LENGTH:Input:45 Counted:46 SEQ:71
L:990 M:252 E: No. of Seq. differs, <211> LENGTH:Input:45 Found:46 SEQ:71
L:995 M:206 E: Mandatory field data missing, <213> ORGANISM
L:1009 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:73

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L:1011 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:73
L:1063 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:74
L:1065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:74
L:1128 M:206 E: Mandatory field data missing, <213> ORGANISM
L:1142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:78
L:1144 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:78
L:1244 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:79
L:1246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:79
L:1324 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:79
L:1327 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:79
L:1401 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:87
L:1409 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:37 SEQ:88
L:1415 M:206 E: Mandatory field data missing, <213> ORGANISM
L:1428 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:708 SEQ:89
L:1433 M:206 E: Mandatory field data missing, <213> ORGANISM
L:1469 M:206 E: Mandatory field data missing, <213> ORGANISM
L:1482 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:708 SEQ:91
L:1487 M:206 E: Mandatory field data missing, <213> ORGANISM
L:1523 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:92